

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2005, 11:53:58 ; Search time 80 Seconds
(without alignments)
742.515 Million cell updates/sec

Title: US-09-824-134-2_COPY_130_245

Perfect score: 593
Sequence: 1 FEAGAAAGAPGEDLCRAAF.....QEVQQAQDLQNRSGAMSPMS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	593	100.0	149	2	Q6LCB0
2	593	100.0	208	1	FADD HUMAN
3	389	65.6	209	2	Q645M6
4	382.5	64.5	205	1	FADD MOUSE
5	382.5	64.5	205	2	Q8CD57
6	381	64.2	208	2	Q8R2E7
7	189	31.9	189	2	Q6Q782
8	115.5	19.5	656	1	R1K1 MOUSE
9	114.5	19.3	1719	2	Q13768
10	114.5	19.3	1856	2	Q99407
11	114.5	19.3	1880	1	ANK1 HUMAN
12	114	19.2	239	2	Q9V3B4
13	112.5	19.0	1848	2	Q61302
14	112.5	19.0	1862	1	ANK1 MOUSE
15	111.5	18.8	671	1	R1K1 HUMAN
16	108.5	18.3	663	2	Q7ZZX8
17	103.5	17.5	461	2	Q96407
18	103	17.4	970	2	Q17342
19	103	17.4	985	2	Q17341
20	103	17.4	1786	2	Q17344
21	103	17.4	1809	2	Q17487
22	103	17.4	1815	2	Q17488
23	103	17.4	1841	2	Q8MQG0
24	103	17.4	1867	2	Q17486
25	103	17.4	2039	2	Q17489
26	103	17.4	6994	2	Q17343
27	103	17.4	6994	2	Q17490
28	96.5	16.3	3924	1	ANK2 HUMAN
29	93	15.7	324	1	TNR6_RAT
30	91.5	15.4	965	2	Q7Z344
31	91.5	15.4	1863	2	Q7Z315

32 91 15.3 343 1 TH01_RAT
33 90.5 15.3 655 2 Q7SYB2
34 90 15.2 186 2 Q7QJ06
35 89.5 15.1 1038 2 Q8OZZ7
36 89.5 15.1 1050 2 Q6PCN2
37 89.5 15.1 1050 2 Q8CCV0
38 89 15.0 293 2 Q919N5
39 87 14.7 332 1 TNR6_PIG
40 87 14.7 1096 2 Q7UQT3
41 86 14.5 143 2 Q7O510
42 86 14.5 811 2 Q9H0P5
43 86 14.5 838 2 Q9CXH1
44 86 14.5 960 2 Q8VDA0
45 86 14.5 1093 2 Q8CBN3

ALIGNMENTS

RESULT 1

Q6LCB0 PRELIMINARY; PRT; 149 AA.
AC Q6LCB0;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE FADD protein (Fragment).
GN Name=FADD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97113335; PubMed=8955195;
RA Kim P.K., Dutra A.S., Chandrasekharappa S.C., Puck J.M.;
RT "Genomic structure and mapping of human FADD, an intracellular
RT mediator of lymphocyte apoptosis."
RL J. Immunol. 157:5461-5466(1996).
DR EMBL, U74301; AAB58483.1;
DR GO; GO:000515; P:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF01335; DED; 1.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50168; DED; 1.
FT NON_TER 1
SQ SEQUENCE 149 AA; 16696 MW; 3D8F7AB866127A41 CRC64;

Query Match 100.0%; Score 593; DB 2; Length 149;

Best Local Similarity 100.0%; Pred. No. 7.9e-47;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEAGAAAGAPGEDLCRAAFNVICDNVGDWRRLARQLKYSDTKIDSIEDRYPNLTERV 60

Db 23 FEAGAAAGAPGEDLCRAAFNVICDNVGDWRRLARQLKYSDTKIDSIEDRYPNLTERV 82

Qy 61 RESLRITWNTKEKNATVAHLVGLRSCQMLVADLVQEVQQAQDLQNRSGAMSPMS 116

Db 83 RESLRITWNTKEKNATVAHLVGLRSCQMLVADLVQEVQQAQDLQNRSGAMSPMS 138

RESULT 2

FADD_HUMAN STANDARD; PRT; 208 AA.
ID FADD_HUMAN
AC Q13156; Q14866;
DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAGAPGEDLCAAFNVICDVGKDWRLARQLKVDTKIDSIDRYPRNLTVERV 60
DB 82 FEAGAAGAPGEDLCAAFNVICDVGKDWRLARQLKVDTKIDSIDRYPRNLTVERV 141
QY 61 RESLRWNTKEKATVAHLVGLRSCQMLVADLVQEQVQARDLQNRSGMSPMS 116
DB 142 RESLRWNTKEKATVAHLVGLRSCQMLVADLVQEQVQARDLQNRSGMSPMS 197

RESULT 3
Q645M6 PRELIMINARY; PRT; 209 AA.
AC Q645M6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Fas-associated via death domain.
GN Name=FADD;
OS Bos taurus (Bovine);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Connor E.E., Sperka M.E., Paape M.J., Williams J.L., Bannerman D.D.;
RT "Cloning and sequencing of the bovine Fas-associated death domain
protein (FADD) cDNA";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sperka M.E., Connor E.E., Paape M.J., Williams J.L., Bannerman D.D.;
RT "Sequencing, chromosomal mapping, and functional characterization of
the bovine Fas-associated death domain (FADD) gene";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN EMBL; AY725483; AAU20801.1;
SQ SEQUENCE 209 AA; 23002 MW; 2EB6BA41F6DB0F9D CRC64;

Query Match 65.6%; Score 389; DB 2; Length 209;
Best Local Similarity 65.5%; Pred. No. 7.1e-28;
Matches 76; Conservative 18; Mismatches 20; Indels 2; Gaps 1;

QY 1 FEAGAAGAPGEDLCAAFNVICDVGKDWRLARQLKVDTKIDSIDRYPRNLTVERV 60
DB 82 FEAGAAGAPGEDLCAAFNVICDVGKDWRLARQLKVDTKIDSIDRYPRNLTVERV 141
QY 61 RESLRWNTKEKATVAHLVGLRSCQMLVADLVQEQVQARDLQNRSGMSPMS 116
DB 142 RELLRWNTKEKATVAHLVGLRSCQMLVADLVQEQVQARDLQNRSGMSPMS 195

RESULT 4
FADD MOUSE
ID FADD MOUSE STANDARD; PRT; 205 AA.
AC Q61160; Q61082;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE FADD protein (FAS-associated death domain-containing protein)
DE (Mediator of receptor induced toxicity).
GN Name=Fadd; Synonyms=Mort1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Winoto A.;
RT "A mouse Fas-associated protein with homology to the human Mort1/FADD

protein is essential for Fas-induced apoptosis";
Mol. Cell. Biol. 16:2756-2763(1996).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96152659; PubMed=8565075; DOI=10.1016/S0092-8674(00)80984-8;
RA Hsu H., Shu H.-B., Pan M.G., Goeddel D.V.;
RT "TRADD-TRAF2 and TRADD-FADD interactions define two distinct TNF
receptor 1 signal transduction pathways";
Cell 84:299-308(1996).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, and Salivary gland;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RP STRUCTURE BY NMR OF 89-183.
RX PubMed=10347191; DOI=10.1074/jbc.274.23.16337;
RA Jeong E.-J., Bang S., Lee T.H., Park Y.-I., Sim W.-S., Kim K.-S.;
RT "The solution structure of FADD death domain. Structural basis of
death domain interactions of Fas and FADD";
J. Biol. Chem. 274:16337-16342(1999).


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DR InterPro; IPF001875; DED.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF01335; DED; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00031; DED; 1.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS0168; DED; 1.
DR PROSITE; PS0168; DED; 1.
SQ SEQUENCE 205 AA; 22891 MW; 4A8DD86B3E08776 CRC64;

Query Match      64.5%; Score 382.5; DB 2: Length 205;
Best Local Similarity 61.7%; Pred. No. 2.8e-27;
Matches 71; Conservative 25; Mismatches 16; Indels 3; Gaps 1

Qy   1  FEAGAAAGAAGEEDLCAAFNVI CDNVCKDWRLRLAKVSDTKIDSTIEDRYPNLTLSRV 60
    ||||| :|||:::||:||||:||||:||||:|:|:||||:||||:|:|:||||:||||:|
Db   82  FEAGTATAPPGAEADLVQAFDVIDCDNVGDWRKLRLARELUKVSSEAKMDGEEKPKRSLSRV 141
    ||||| :|||:::||:||||:||||:||||:|:|:||||:||||:|:|:||||:||||:|

Qy   61  RESLRIRWNTKEKENTAVHVLGYALRSQCMNLVDLVQEVQQARDQNLRSGAMSPM 115
    ||||| :|||:::||:||||:||||:||||:|:~::~|||:||||:||||:|
Db   142  RESLUKWNAEKKNASVAGLVKALTCTNLNLVDLVVEEAQRS---VSKSENNSPV 193
    ||||| :|||:::||:||||:||||:||||:|:~::~|||:||||:||||:|
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RESULT 6		
Q8R2E7	PRELIMINARY;	PRT; 208 AA.
ID	Q8R2E7	
AC	Q8R2E7;	
DT	01-JUN-2002 (TrEMBLrel. 21, Created)	
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Fas death domain associated protein (FADD/MORT1 protein with death effector domain).	
DE	Name=fadd;	
GN	Rattus norvegicus (Rat).	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus	
OX	NCBI_TaxID=10116;	
(1)		
RN	SEQUENCE FROM N.A.	
RP	STRAIN=Sprague-Dawley; TISSUE=Ischemic brain;	
RC	Spadoni C.G.;	
RA	"Identification of neuronal caspases and involvement of death domain proteins in neuronal apoptosis."	
RT	Thesis (2001), University of London, United Kingdom.	
RL	(2)	
RN	SEQUENCE FROM N.A.	
RP	STRAIN=Sprague-Dawley; TISSUE=Ischemic brain;	
RC	Neame S.;	
RA	Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.	

SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=22254898; PubMed=12167637; DOI=10.1074/jbc.M203484200;
Kim P.K., Wang Y., Gambotto A., Kim Y.M., Weller R.,
Zuckerbraun B.S., Hua Y., Watkins S.C., Billiar T.R.;
Hepatocyte Fas-associating death domain protein/mediator of receptor-
induced toxicity [FADD/MORT1] levels increase in response to pro-
apoptotic stimuli.";
J. Biol. Chem. 277:38855-38862(2002).
[4]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Liver;
Kim P.K., Billiar T.R.;
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AJ441127; CAD29628.1; -;
EMBL: AF406779; AN01113.1; -;
HSP: Q61160; IFAD.
GO: GO:0005515; F:protein binding; IEA.
GO: GO:0042981; P:regulation of apoptosis; IEA.
GO: GO:0007165; P:signal transduction; IEA.
InterPro: IPR000488; Death.
InterPro: IPR011029; DEATH_like.
InterPro: IPR01875; DED.
Pfam: PF00531; Death; 1.

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DR Pfam: PF01335; DED; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00031; DED; 1.
DR PROSITE: PSS0047; DEATH_DOMAIN; 1.
DR PROSITE: PSS0168; DED; 1.
DR SQ SEQUENCE 208 AA; 23124 MW; ABA3305406137CDB CRC64;

Query Match      64.2%; Score 381; DB 2; Length 208;
Best Local Similarity 64.2%; Pred. No. 3.9e-27;
Matches 70; Conservative 21; Mismatches 18; Indels 0; Gaps 0;

Qy   1 FEAGAAAGAAGGEDLCAAFNVICDNGVKDWRLARLVKVDTKIDSIDIEDYPRNLTERV 60
Db   82 FEAGTAATPTGGEADLFVAFDIICDNNVGROWKLARELKIVSEAKIDGIEIKRPSLSRV 141

Qy   61 RESLRIRWNTKEKENATVAHLVLGARLSQQMNLVADVLOVEQQOARDLONRS 109
Db   142 PETTFRVMKNVKEKNASVAGLVKALACRLNVLADVLEALMAOGSVSKS 190
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RESULT 7
ID Q6Q782 PRELIMINARY; PRT; 189 AA.
AC Q6Q782;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Fas-associated death domain.
OS Itcalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20069572; PubMed=10602874; DOI=10.1007/s002510050588;
RA Hawke N.A., Yoder J.A., Litman G.W.;
RT "Expanding our understanding of immunoglobulin, T-cell antigen
RT receptor, and novel immune-type receptor genes: a subset of the
RT immunoglobulin gene superfamily.";
RL Immunogenetics 50:124-133(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX Long S., Wilson M.R., Bengten E., Hawke N.A., Miller N.W.,
RA Chinchur V.G.;
RT Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RN [3]

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DR HSSP; Q13158; IAIW.
DR GO; GO:0005515; P:protein binding; IEA.
DR GO; GO:0042961; P:regulation of apoptosis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPRO00488; Death.
DR InterPro; IPRO11029; DEATH_like.
DR InterPro; IPRO01875; DEB.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF01335; DEB; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00031; DEB; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS0168; DEB; 1.
DR PROSITE; PS0168; DEB; 1.
SQ SEQUENCE 189 AA; 22240 MW; 63E85PAD3D2E1A9 CRC64;

Query Match      31.9%; Score 189; DB 2; Length 189;
Best Local Similarity 39.6%; Pred.No.1.7e-09;
Matches 38; Conservative 22; Mismatches 32; Indels 4; Gaps 2

'Qy' 7          11 PGE---EDLCAAFNVICDNVGKDWRRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIW 67
                | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
91 PNEYELEKINCAIEVISQLGRKWIKYGRKLKIARTKLEGIOEKHPRNLEEQVREWFKEW 150

Db              68 KNTKENATVAHLGALRSQQMNLVADLVQ-EVQQA 102
                | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
151 MCHHKAERAKVDIELIRALRDCTLTNYTADVVMNLOKA 186

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RA	Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinieki M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC	-I- FUNCTION: Promotes apoptosis and activation of NF-kappa-B.
CC	Required for TNFRSF1A mediated activation of NF-kappa-B.
CC	-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC	-I- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds RIPK3, UBCE1P1, EGFR, IKBKKG, TRAF1, TRAF2 and TRAF3. Interacts with BNIP1 (By similarity).
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic.
CC	-I- TISSUE SPECIFICITY: Found at low levels in all tissues.
CC	-I- INDUCTION: In concanavalin A-treated splenocytes.
CC	-I- PTM: Proteolytically cleaved by caspase-8 during TNF-induced apoptosis. Cleavage abolishes NF-kappa-B activation and enhances pro-apoptotic signaling through the TRADD-FADD interaction (By similarity).
CC	-I- PTM: Autophosphorylated on serine and threonine residues (By similarity).
CC	-I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC	-I- SIMILARITY: Contains 1 death domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; U25995; AAB60487.1; --
DR	EMBL; AK030959; BAC27194.1; --
DR	EMBL; BC050905; AAH50905.1; ALT_INIT.
DR	EMBL; BC054542; AAH54542.1; --
DR	EMBL; BC058162; AAH58162.1; --
DR	PIR; I49299; I49299.
DR	HSPG; QJ3158; IE41.
DR	MGI; 108212; Ripk1.
DR	InterPro; IPR000488; Death.
DR	InterPro; IPR011029; DEATH like.
DR	InterPro; IPR011009; Kinase like.
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR008271; Ser_thr_pkin_AS.
DR	InterPro; IPR001245; Tyr_pkinase.
DR	Pfam; PF00531; Pkinase; 1.
DR	PRINTS; PR00109; TYRKINASE.
DR	ProDom; PD000001; prot_kinase; 1.
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS50108; PROTEIN_KINASE_ST; 1.
DR	KW Apoptosis; ATP-binding; Serine/threonine-protein kinase; Transferase.
FT	DOMAIN 17 290 Protein kinase.
FT	NP_BIND 23 31 ATP (By similarity).
FT	BINDING 46 46 ATP (By similarity).
FT	ACT_SITE 138 138 Proton acceptor (By similarity).
FT	DOMAIN 569 654 Death.
FT	VARIANT 473 473 T -> I.
FT	CONFLICT 66 66 M -> K (in Ref. 2).
SQ	SEQUENCE 656 AA; 74854 MW; ABB350B523879933 CRC64;
	Query Match 19.5%; Score 115.5; DB 1; Length 656;
	Best Local Similarity 34.9%; Pred. No. 0.04; Indels 3; Gaps 3;
	Matches 29; Conservative 22; Mismatches 29;
QY	21 NVICDNVGDWRRLARQLKVSDETRYSIDEDRPYN-LTERVRESLR1WKNTA-KENATVA 78 : : : : : : : :

Db 573 NPIRENLGROWKNCARKLFTESQIDEIDHYDRLGKVKYQMLQKWLMBRTGKATVG 632

Qy 79 HLVGAL-RSQMNLVADLVQEVQ 100

Db 633 KLAQALHQCRRIDLLNHLIRASQ 655

RESULT 9

Q13768 PRELIMINARY; PRT: 1719 AA;
 ID Q13768
 AC Q13768;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Alt. ankyrin (Variant 2.2).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hematopoietic;
 RX MEDLINE=90158830; PubMed=2137557;
 RA Lux S.E., John K.M., Bennett V.;
 RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
 RT structure with homology to tissue-differentiation and cell-cycle
 RT control proteins".
 RL Nature 344:36-42(1990).
 DR EMBL; X16609; CAA34611.1; -.
 DR HSSP; P16157; IN11.
 DR GO; GO:0016323; C:basolateral plasma membrane; ISS.
 DR GO; GO:0005856; C:cytoskeleton; NAS.
 DR GO; GO:0008093; F:cytoskeletal adaptor activity; ISS.
 DR GO; GO:0019899; F:enzyme binding; ISS.
 DR GO; GO:0030507; F:spectrin binding; ISS.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
 DR GO; GO:006887; F:exocytosis; NAS.
 DR GO; GO:0045199; P:maintenance of epithelial cell polarity; ISS.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR00906; ZU5.
 DR Pfam; PF00023; Ank; 23.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 23.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 20.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW ANK repeat.
 SQ SEQUENCE 1719 AA; 189010 MW; F63465D16D975CBF CRC64;

Query March 19.3%; Score 114.5; DB 2; Length 1719;
 Best Local Similarity 28.1%; Pred. No. 0.14; Indels 7; Gaps 2;
 Matches 32; Conservative 26; Mismatches 49

Qy 8 GAAPGEEDLCAAFNVICDNVGVKWRRLARQLKVSDTKIDSDIEDYPRNLTFRVRESLRW 67
 Db 1395 GSLSGTEQAENKMAVISEHGLSWAELARELOFSVEDINRVRVENPSLLEQSVALLNLW 1454
 Qy 68 KNTKENATVAHLVGLRSCQMNVLVDLVQ-EVQQRDLQ-----NRSGAMSP 114
 Db 1455 VIREQONAMENLYALQSIDRGEIVNNLEGSQRNLKPKDRRHTDRDYSLSP 1508

RESULT 10

Q99407 PRELIMINARY; PRT: 1856 AA.
 ID Q99407
 AC Q99407;
 DT 01-MAY-1997 (TRENBLrel. 03, Created)

DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Ankyrin.
 GN Name=ANK1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97382244; PubMed=9235914; DOI=10.1074/jbc.272.31.19220;
 RA Callagher P.G., Tse W.T., Scarpa A.L., Lux S.E., Forget B.G.;
 RT "Structure and organization of the human ankyrin-1 gene. Basis for
 RT complexity of pre-mRNA processing".
 RL J. Biol. Chem. 272:19220-19228(1997).
 DR EMBL; U50092; AAB47805.1; JOINED.
 DR EMBL; U50093; AAB47805.1; JOINED.
 DR EMBL; U50094; AAB47805.1; JOINED.
 DR EMBL; U50095; AAB47805.1; JOINED.
 DR EMBL; U50096; AAB47805.1; JOINED.
 DR EMBL; U50097; AAB47805.1; JOINED.
 DR EMBL; U50098; AAB47805.1; JOINED.
 DR EMBL; U50099; AAB47805.1; JOINED.
 DR EMBL; U50100; AAB47805.1; JOINED.
 DR EMBL; U50101; AAB47805.1; JOINED.
 DR EMBL; U50102; AAB47805.1; JOINED.
 DR EMBL; U50103; AAB47805.1; JOINED.
 DR EMBL; U50104; AAB47805.1; JOINED.
 DR EMBL; U50105; AAB47805.1; JOINED.
 DR EMBL; U50106; AAB47805.1; JOINED.
 DR EMBL; U50107; AAB47805.1; JOINED.
 DR EMBL; U50108; AAB47805.1; JOINED.
 DR EMBL; U50109; AAB47805.1; JOINED.
 DR EMBL; U50110; AAB47805.1; JOINED.
 DR EMBL; U50111; AAB47805.1; JOINED.
 DR EMBL; U50112; AAB47805.1; JOINED.
 DR EMBL; U50113; AAB47805.1; JOINED.
 DR EMBL; U50114; AAB47805.1; JOINED.
 DR EMBL; U50115; AAB47805.1; JOINED.
 DR EMBL; U50116; AAB47805.1; JOINED.
 DR EMBL; U50117; AAB47805.1; JOINED.
 DR EMBL; U50118; AAB47805.1; JOINED.
 DR EMBL; U50119; AAB47805.1; JOINED.
 DR EMBL; U50120; AAB47805.1; JOINED.
 DR EMBL; U50121; AAB47805.1; JOINED.
 DR EMBL; U50122; AAB47805.1; JOINED.
 DR EMBL; U50123; AAB47805.1; JOINED.
 DR EMBL; U50124; AAB47805.1; JOINED.
 DR EMBL; U50125; AAB47805.1; JOINED.
 DR EMBL; U50126; AAB47805.1; JOINED.
 DR EMBL; U50127; AAB47805.1; JOINED.
 DR EMBL; U50128; AAB47805.1; JOINED.
 DR EMBL; U50129; AAB47805.1; JOINED.
 DR EMBL; U50130; AAB47805.1; JOINED.
 DR EMBL; U50131; AAB47805.1; JOINED.
 DR EMBL; U50132; AAB47805.1; JOINED.
 DR HSSP; P16157; IN11.
 DR GO; GO:0016323; C:basolateral plasma membrane; ISS.
 DR GO; GO:0008093; F:cytoskeletal adaptor activity; ISS.
 DR GO; GO:0019899; F:enzyme binding; ISS.
 DR GO; GO:0030507; F:spectrin binding; ISS.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
 DR GO; GO:0045199; P:maintenance of epithelial cell polarity; ISS.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR00906; ZU5.
 DR Pfam; PF00023; Ank; 22.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 22.
 DR SMART; SM00005; ZU5.


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FT REPEAT 666 695 ANK 20.
FT REPEAT 699 728 ANK 21.
FT REPEAT 732 761 ANK 22.
FT REPEAT 765 794 ANK 23.
FT DOMAIN 1402 1486 Missing (in isoform 2).
FT VARSPLIC 1512 1873 /FTid=VSP_000264.
FT VARSPLIC 1874 1874 H -> D (in isoform 2).
FT VARSPLIC 1874 1874 /FTid=VSP_000265.
FT VARSPLIC 1849 1880 TWGPLEDSELEVDIDYFMKHSKDHSTPNP -> ELRGS
FT GLQDLEIEGRKGAQIVKVASLKRKQ (in isoform
FT 3).
FT /FTid=VSP_000266.
FT R -> T.
FT /FTid=VAR_000595.
FT V -> I (in HS).
FT /FTid=VAR_000596.
FT R -> H (in Brueggen).
FT /FTid=VAR_000597.
FT V -> A.
FT /FTid=VAR_000598.
FT D -> E.
FT /FTid=VAR_000599.
FT E -> D.
FT /FTid=VAR_000601.
FT S -> T.
FT /FTid=VAR_000600.
FT D -> N (in Duesseldorf).
FT /FTid=VAR_000602.
FT R -> D.
FT /FTid=VAR_000603.
FT A -> S (in Ref. 2).
FT V -> I (in Ref. 2).
FT CONFLICT 229 229
FT CONFLICT 1545 1545
FT SEQUENCE 1880 AA; 206145 MW; 1CSF5E7EFD1CD428 CRC64;
Query Match 19.3%; Score 114.5; DB 1; Length 1880;
Best Local Similarity 28.1%; Pred. No. 0.16;
Matches 32; Conservative 26; Mismatches 49; Indels 7; Gaps 2;
Qy 8 GAMPGEEDLCANFVNCVGVKWRRLARQLKVSQTDKIDIEDYPRNLTVRESRIW 67
Db 1394 GSLSTGEQEMKMAVISEHGLSMAELRLQFSVEDINRVENPSLLEQSVALLNLW 1453
Qy 68 KNTKEKATVAHLGALRSQMNVLADLVQ-EVQARDLQ-----NRSGAMSP 114
Db 1454 VIREGQANMENLYTQSIDRGEIVNMLESGRQSRNLKPDPRHRTDYSLS 1507
RESULT 12
Q9V3B4 PRELIMINARY; PRT; 239 AA.
AC Q9V3B4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG12297-PA (Death domain-containing adaptor protein) (Death-domain
DE containing protein Bc4).
GN Name=BC4; ORFNames=CG12297;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherv J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris K.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195 (2000).
[2]
SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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RN  [7]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20469420; PubMed=10934188; DOI=10.1074/jbc.C000341200;
RA  Hu S., Yang X.;
RT  "afADP, a novel death domain-containing adapter protein for the
RL  Drosophila caspase DREDD.";
RN  J. Biol. Chem. 275:30761-30764(2000).
RN  [8]
RP  SEQUENCE FROM N.A.
RA  Zhou L., Steller H.;
RL  Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR  ENBL; AS003737; AAF55950.1; -
DR  ENBL; AF295103; AAG22535.1; -
DR  ENBL; AF222005; AAF44325.1; -
DR  HSP; O61160; 1FAD.
DR  Intact; Q9V3B4; -
DR  FlyBase; FBgn0038928; BG4.
DR  GO; GO:000515; F:protein binding; TAS.
DR  GO; GO:0050829; P:defense response to Gram-negative bacteria; TAS.
DR  GO; GO:0006955; P:immune response; IMP.
DR  GO; GO:0007291; P:sperm individualization; IMP.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR011029; DEATH_like.
DR  Pfam; PF00531; Death; 1.
DR  PROSITE; PS0017; DEATH_DOMAIN; 1.
SQ  SEQUENCE 239 AA; 27421 MW; F43CFAA546C3FCD9 CRC64;

Query Match 19.2%; Score 114; DB 2; Length 239;
Best Local Similarity 26.8%; Pred. No. 0.018;
Matches 34; Conservative 22; Mismatches 37; Indels 34; Gaps 4;

QY 3 AGAAGAAGGERDLCAA-----FNVTCDNVGKDWRRRLARQLK 39
Db 115 APASQAQPSVSELAAPPTAIQNYATPAFTDKRTWPKISBELGRYWRRLGSAG 174
QY 40 VSDTKIDIEDRYPRNLTERVRESLRINWTKENK-----TVHLGALRSQMNVLAD 94
Db 175 IEGQMDTEERYPHDLKSQI---LRLQLIEEDDCHDKPHFLRLCRALGDCGRN---D 228
QY 95 LVQEVQQ 101
Db 229 LKRVQE 235

RESULT 13
Q61302
ID Q61302 PRELIMINARY; PRT; 1848 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Erythroid ankryrin.
GN Name=Ank1; Synonyms=Ank-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Neural;
RX MEDLINE=91252825; PubMed=8486643;
RA Birkenmeier C.S., White R.A., Peters L.L., Hall E.J., Lux S.E.,
RA Barker J.E.;
RT "Complex patterns of sequence variation and multiple 5' and 3' ends
RT are found among transcripts of the erythroid ankryrin gene.";
RL J. Biol. Chem. 268:9533-9540(1993).
DR EMBL; X69063; CAA48801.1; -
DR FIR; S37771; S37771.
DR HSP; P16157; IN11.
DR MGD; MGI:88024; Ank1.
DR GO; GO:0016323; C:basolateral plasma membrane; ISS.
DR GO; GO:0008093; F:cytoskeletal adaptor activity; ISS.
DR GO; GO:0019899; F:enzyme binding; ISS.

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DR GO; GO:0030507; F:spectrin binding; ISS.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
DR GO; GO:0045199; P:maintenance of epithelial cell polarity; ISS.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR000906; ZUS_.
DR Pfam; PF00023; Ank; 23.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00791; ZUS; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 23.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZUS; 1.
DR PROSITE; PS00088; ANK_REPEAT; 20.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
KW ANK repeat.
SQ SEQUENCE 1848 AA; 202576 MW; 5744BECBF9EBA056 CRC64;

Query Match 19.0%; Score 112.5; DB 2; Length 1848;
Best Local Similarity 29.0%; Pred. No. 0.24;
Matches 29; Conservative 27; Mismatches 37; Indels 7; Gaps 2;

QY 22 VICDNVGVKDWRRRLARQLKVSDDTKIDSDRYPRNLTERVRESLRINWTKENKATVAHLV 81
Db 1421 VIREHGLSWAELARELQSFVEDINRIVENPNSLLDQSTALLTLWVDREGENAKMENLY 1480
QY 82 GALSRCOMNLVADLVQ-EVQQAARDLQ-----NRSGAMSP 114
Db 1481 TALNRNDRSEIVNMLEVSGRQSRNLKPERRHGRDREYSLSP 1520

RESULT 14
ANK1_MOUSE
ID ANK1_MOUSE STANDARD; PRT; 1862 AA.
AC Q02357;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ankryrin 1 (Erythrocyte ankryrin).
GN Name=Ank1; Synonyms=Ank-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Erythrocyte;
RX MEDLINE=92345717; PubMed=1386265;
RA White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;
RT "Murine erythrocyte ankryrin cDNA: highly conserved regions of the
RT regulatory domain.";
RL Mamm. Genome 3:281-285(1992).
CC -!- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC elements; bind to the erythrocyte membrane protein band 4.2, to
CC Na-K ATPase, to the lymphocyte membrane protein gp85, and to the
CC cytoskeletal proteins fodrin, tubulin, vimentin and desmin.
CC Erythrocyte ankryrins also link spectrin (beta chain) to the
CC cytoplasmic domain of the erythrocytes anion exchange protein;
CC they retain most or all of these binding functions.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic surface of erythrocytic plasma
CC membrane.
CC -!- PTM: Regulated by phosphorylation (By similarity).
CC -!- PTM: Acylated by palmitic acid group(s) (By similarity).
CC -!- SIMILARITY: Contains 23 ANK repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC	EMBL; M84756; AAA37236.1; -	
CC	PIR; I49502; I49502.	
DR	HSSP; P16157; IN11.	
DR	MGI; M84756; AAA37236.1; -	
DR	GO; GO:0016323; Cytoskeletal adaptor activity; ISS.	
DR	GO; GO:0008093; F-actin binding; ISS.	
DR	GO; GO:0019899; F-actin binding; ISS.	
DR	GO; GO:0030507; F-actin binding; ISS.	
DR	GO; GO:0052000; F-actin binding; ISS.	
DR	GO; GO:0045199; F-actin binding; ISS.	
DR	InterPro; IPR002110; ANK.	
DR	InterPro; IPR000488; Death.	
DR	InterPro; IPR011029; DEATH_like.	
DR	InterPro; IPR000906; ZU5.	
DR	Pfam; PF00023; ANK; 23.	
DR	Pfam; PF00531; Death; 1.	
DR	Pfam; PF00791; ZU5; 1.	
DR	PRINTS; PR01415; ANKYRIN.	
DR	SMART; SM00248; ANK; 23.	
DR	SMART; SM00005; DEATH; 1.	
DR	SMART; SM00218; ZU5; 1.	
DR	PROSITE; PS02827; ANK_REPEAT; 1.	
DR	PROSITE; PS00088; ANK_REPEAT; 20.	
DR	PROSITE; PS00017; DEATH_DOMAIN; 1.	
KW	ANK repeat; Cytoskeleton; Lipoprotein; Phosphorylation; Repeat.	
FT	DOMAIN 1 827	
FT	828 1386	
FT	1387 1862	
FT	DOMAIN	
FT	40 69	
FT	73 102	
FT	106 135	
FT	139 168	
FT	170 197	
FT	201 230	
FT	234 263	
FT	267 296	
FT	300 329	
FT	333 362	
FT	366 395	
FT	399 428	
FT	432 461	
FT	465 494	
FT	498 527	
FT	531 560	
FT	564 593	
FT	597 626	
FT	630 659	
FT	663 692	
FT	696 725	
FT	729 758	
FT	762 791	
FT	1399 1483	
SQ	SEQUENCE 1862 AA; 204242 MW; AE6B85B5B29001E5 CRC64;	
Query Match	19.0%; Score 112.5; DB 1; Length 1862;	
Best Local Similarity	29.0%; Pred. No. 0.24; 37; Indels 2;	
Matches	29; Conservative 27; Mismatches 7; Gaps 2;	
Qy	22 VICNVGDMRLARQLKVSPTKIDSTEDYPRNLTRVRSRLRWKNTKENTAVHLV 81	
Db	1405 VIREHGLSWALEARELOFSVEDINRTEVENPSLLDQSTALLTLWDREGENAKMENLY 1464	
Qy	82 GALSRCQMNVLVADLVQ-EVQQRDLQ-----NFGSGMSP 114	
Db	1465 TALNRIDRSEIVNMLEGSGRQSRNLKPRRRHGDREYSLSLP 1504	

RESULT 15	
ID	RIK1 HUMAN
AC	Q13546; Q13180;
DT	01-NOV-1997 (Rel. 35, Created)
DT	30-NOV-2000 (Rel. 39, Last sequence update)
DE	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Receptor-interacting serine/threonine-protein kinase 2 (EC 2.7.1.37)
DE	(serine/threonine-protein kinase RIP) (Cell death protein RIP)
DE	(Receptor-interacting protein).
GN	Name=RIK1; Synonyms=RIP;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]_TaxID=9606;
RP	SEQUENCE FROM N.A., AUTOPHOSPHORYLATION, MUTAGENESIS OF LYS-45, AND
RP	INTERACTIONS WITH TRADD; TRAF1; TRAF2 AND TRAF3.
RC	TISSUE=Umbilical vein endothelial cells;
RX	MEDLINE=96200892; PubMed=8612133; DOI=10.1016/S1074-7613(00)80252-6;
RA	Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;
RT	"TNF-dependent recruitment of the protein kinase RIP to the TNF
RT	receptor-1 signaling complex.";
RL	Immunity 4:387-396(1996).
RN	[2]
RP	REVISION TO 120.
RA	Huang J., Hsu H., Baichwal V.R., Goeddel D.V.;
RL	Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
[3]	SEQUENCE FROM N.A.
RN	RA Sycamore N.;
RP	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RC	TISSUE=Leukemic T-cell;
RX	MEDLINE=95277838; PubMed=7538908; DOI=10.1016/0092-8674(95)90072-1;
RA	Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
RT	"RIP: a novel protein containing a death domain that interacts with
RT	Fas/APO-1 (CD95) in yeast and causes cell death.";
RL	Cell 81:513-523(1995).
RN	[5]
RP	CLEAVAGE BY CASPASE-8, AND MUTAGENESIS OF ASP-324.
RX	MEDLINE=99452794; PubMed=10521396; DOI=10.1101/gad.13.19.2514;
RA	Lin Y., Devin A., Rodriguez Y., Liu Z.-G.;
RT	"Cleavage of the death domain kinase RIP by caspase-8 prompts TNF-
RT	induced apoptosis.";
RL	Genes Dev. 13:2514-2526(1999).
RN	[6]
RP	INTERACTION WITH RIPK3.
RX	MEDLINE=99287880; PubMed=10358032; DOI=10.1074/jbc.274.24.16871;
RA	Sun X., Lee J., Navas T., Baldwin D.T., Stewart T.A., Dixit V.M.;
RT	"RIP3, a novel apoptosis-inducing kinase.";
RL	J. Biol. Chem. 274:16871-16875(1999).
RN	[7]
RP	INTERACTION WITH BNL1.
RX	MEDLINE=99340272; PubMed=10409763;
RA	Izumi K.M., Cahir McFarland E., Ting A.T., Riley E.A., Seed B.,
RA	Kieff E.D.;
RT	"The Epstein-Barr virus oncoprotein latent membrane protein 1 engages
RT	the tumor necrosis factor receptor-associated proteins TRADD and
RT	receptor-interacting protein (RIP) but does not induce apoptosis or
RT	require RIP for NF-kappaB activation.";
RL	Mol. Cell. Biol. 19:5759-5767(1999).
RN	[8]
RP	INTERACTION WITH IKKb.
RX	MEDLINE=99128359; PubMed=9927690; DOI=10.1073/pnas.96.3.1042;
RA	Li Y., Kang J., Friedman J., Tarassishin L., Ye J., Kovalenko A.,
RA	Wallach D., Horvitz M.S.;
RT	"Identification of a cell protein (FIP-3) as a modulator of NF-kappaB
RT	activity and as a target of an adenovirus inhibitor of tumor necrosis
RT	factor alpha-induced apoptosis.";
RL	Proc. Natl. Acad. Sci. U.S.A. 96:1042-1047(1999).
RN	[9]

INTERACTION WITH EGFR.
RX MEDLINE=21153697; PubMed=11116146; DOI=10.1074/jbc.M008458200;
RA Habib A.A., Chatterjee S., Park S.-K., Ratan R.R., Lefebvre S.,
RA Vartanian T.,
RT "The epidermal growth factor receptor engages receptor interacting
RT protein and nuclear factor-kappa B (NF-kappa B)-inducing kinase to
RT activate NF-kappa B. Identification of a novel receptor-tyrosine
RT kinase signalosome.";
RL J. Biol. Chem. 276:8865-8874 (2001).
RN [10]
RX INTERACTION WITH UBC7P1P1.
RX MEDLINE=21975204; PubMed=11854271; DOI=10.1074/jbc.M108675200;
RA Chen D., Li X., Zhai Z., Shu H.-B.,
RT "A novel zinc finger protein interacts with receptor-interacting
RT protein (RIP) and inhibits tumor necrosis factor (TNF)- and IL1-
RT induced NF-kappa B activation";
RL J. Biol. Chem. 277:15985-15991 (2002).
CC -!- FUNCTION: Promotes apoptosis and activation of NF-kappa-B.
CC Required for TNFRSF1A mediated activation of NF-kappa-B.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is
CC recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds
CC RIPK3, UBC7P1P1, EGFR, IKKSG, TRAF1, TRAF2 and TRAF3. Interacts
CC with BNLF1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: Proteolytically cleaved by caspase-8 during TNF-induced
CC apoptosis. Cleavage abolishes NF-kappa-B activation and enhances
CC pro-apoptotic signaling through the TRADD-PADD interaction.
CC -!- PTM: Autophosphorylated on serine and threonine residues.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -----
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CC -----
DR EMBL; U50062; AAC32232.1; -;
DR EMBL; AL031963; CAD70625.1; -;
DR EMBL; U25994; AAC50137.1; -;
DR FIR; T09479; T09479.
DR HSP; P41240; 1BYG.
DR Genew; HGNC:10019; RIPK1.
DR MIM; 603453; -;
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; IEP.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IEP.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Apoptosis; ATP-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
DOMAIN 17 289
NP_BIND 23 31 Protein kinase.
FT BINDING 49 49 ATP (By similarity).
FT ACT_SITE 138 138 ATP (By similarity).
FT ACT_SITE 138 138 Proton acceptor (By similarity).
DOMAIN 583 669 Death.

FT	DOMAIN	411	414	Poly-Arg.
FT	SITE	324	325	Cleavage (by caspase-8).
FT	MUTAGEN	45	45	K->A: Abolishes kinase activity.
FT	MUTAGEN	324	324	D->K: Abolishes cleavage by caspase-8.
FT	CONFLICT	438	438	V -> A (in Ref. 3).
FT	CONFLICT	514	514	T -> S (in Ref. 4).
SQ	SEQUENCE	671 AA;	75958 MW;	BADC4E7E70456ABE CRC64;

Query Match 18.8%; Score 111.5; DB 1; Length 671;
Best local similarity 36.4%; Pred. No. 0.095;
Matches 28; Conservative 19; Mismatches 27; Indels 3; Gaps 3;

QY	23	ICDNVGVKDWERLARQLKVKVSDTKIDSDYRPN-LTERVESLRWKNTK-ENATVAHL	80
Db	590	IRENLGKHWNKCARLQFTQSQIDEIDHDYERDLGKVKYQMLQKQWVRREGIKATVGKL	649

QY	81	VGALRSC-QMNLVADLV	96
Db	650	AQALHQCSRIDLSSLI	666

Search completed: February 11, 2005, 16:43:05
Job time : 84 secs